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cyno3-16 cDNA nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCGTGGAATCAGGC
TCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAAAAACATGTGGTGGTGGCAGCAAACCTCCC
ACGTGCCACCGTGCCAGCACCTGAATCCTGGGGGGACCGTCAGTCTTCCCTCTTCCCCCAAAA
CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTAGACGTGAGCCAG
GAAGACCCCGATGTCAAGTTCAACTGGTACGTAAATGGCGCGGAGGTGCATCATGCCAGACGAAG
CCACGGGAGACGCAGTACAACAGCACATATCGTGTGGTCAGCGTCCTCACCCTCACGCACCAGGAC
TGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAA
ACCATCTCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGGGAG
GAGCTGACCAAGAACCAGGTACGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTC
GTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCC
GACGGCTCCTACTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCT
CCGGGTAAA (SEQ ID NO. 1)

cyno3-16 amino acid sequence

ASTKGPSVFP LAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGSLTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEIKTCGGGSKPPTCPPCPAPELLGGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSQEDPDVKFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQD
WLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIV
VEWESSGPENTYKTPPVLDSDGSYFLYSLKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLS
PGK (SEQ ID NO. 2)

FIG. 1

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cyno33 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCTTGCTCCAGGAGCACCTCCCAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTTCGTGGAACTCAGGC
GCCCTGACCAGCGGCGTGACACCTTCCAGGCTGTCTACAGTCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACTCAGACCTACGTCTGCAACGTCGTTTCATGAG
CCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCGAGGGAAGGGGGGTGTCTGCTG
GAAGCCAGGCTCGGCCCTCCTGCCTGGACAACTCTGGCTGTGTCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCCGTCTGTCTTCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC
TTCTGGCTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCCTACCCAGGCCCTGCACA
CACAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA
AGCCCAACCCAAAGGCCAACTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCACATCCCAGT
AACTCCCAATCTTCTCTCTGTCAGGGCTCCCATGTCTGTTCCACGTGCCACCGTGCCAGGTAAGCC
AGCCAGGCCTCACCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA
GGCCCTGCCCCGGGTGCTGACACGTCCACCTCCATCTCTTCTCAGCTGAACTCCTGGGGGGACCGT
CAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATTTCCCGGACCCCTGAGGTCACGT
GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCACAATGCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG
TCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAG
CCCTCCCGGCCCAAGCAGAAAACCTGTCTCCAAAACCAAGGTGGGACCCGCGGGGCACGAGGGC
CACGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC
CCTACAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAG
AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGCG
AGCAACGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGTGGACTCCGACGGCTCCTAC
TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA
(SEQ ID NO. 3)

cyno33 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKTVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY
TCKVSNKALPAPKQKTIVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIIVEWASNG
QPENTYKTTTPVLDSDGSYFLYSKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK
(SEQ ID NO. 4)

FIG. 2

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cyno2-4 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCTCCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACTGTGTTCGTGGAACCTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCCGGTGTCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTCATGAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGAGGGGGAGTGTCTGCTG
GAAGCCATGCTCGGCCCTCCTGCCTGGACAAACCCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCGGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGACAGTC
TTCTGGCTTTTTCCACCAGACTCCGAGCAGGCACAGGCTGGATGCCCCTACCCCAAGGCTCTGCACA
CATAGGGGCTGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCCTGCTCCTGACCT
AAGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCGGAAACCTTCTCTCCTACCAGATCCCAG
TAACTCCCAATCTTCTCTCTGTCAGAGTTTACACCCCCATGCCACCATGCCAGGTAAGCCAGCCC
AGGCCTCGCCCTCCAGCTCAAGGTGGGACAAGTGCCCTAGAGTGGCCTGTGTCCAGGGACAGGCCC
CGCCTGGGTGCTGACATGCCACCTCCATCTCTTCTCAGCACCTGAACTCCTGGGGGGACCGTCA
GTCTTCTCTTCCCCCCTAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAG
GTGCATCATGCCCAGACGAAGCCACGGGAGAGGCAGTTCAACAGCACGTACCGCGTGGTCAGCGTC
CTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGC
CTCCCGGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGTGGGACCCGCGGGGGCCCGAGGGCCA
CGTGGACAGAGGCCGGCTCAGCCCACCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC
TACAGGGCAGCCCCGAGAGCCGCAGGTGTACATCCTGCCCCGCCCCAGGAGGAGCTGACCAAGAA
CCAGGTCAGCCTGACCTGCCTGGTCACAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAG
CAACGGGCAGCCGGAGAACACCTACAAGACCACCCGCCCCGTGCTGGACTCCGACGGCTCCTACTT
CCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGT
GATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAA

(SEQ ID NO. 5)

cyno2-4 amino acid sequence

ASTKGPSVFPLASSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTPPCPPCPAPELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWLNGKEYT
CKVSNKGLPAPIEKTISKAKGQPREPQVYILPPPQEELTKNQVSLTCLVTGFYPSDIAVEWESNGQ
PENTYKTTTPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSLSPGK

(SEQ ID NO. 6)

FIG. 3

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cyno2-4cys genomic nucleotide sequence

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCTTGCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACTGTGTCGTGGAACCTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTTCGTTTCATGAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGAGGGGGAGTGTCTGCTG
GAAGCCATGCTCGGCCCTCCTGCCTGGACAAACCCCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCCGGTCTGTCTCCTCAGGAGGCTCTGCCCACCCCACTCATGCTCAGGGAGACAGTC
TTCTGGCTTTTTCCACCAGACTCCGAGCAGGCACAGGCTGGATGCCCCACCCCAAGGCTCTGCACA
CATAGGGGCTGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCTCCTGACCT
AAGCCCACCCCAAAGGCCAACTCCACTCCCTCAGCTCGGAAACCTTCTCTCCTACCAGATCCCAG
TAACTCCCAATCTTCTCTCTGCAGAGTTACACCCCCCATGCCCACCATGCCCAGGTAAGCCAGCCC
AGGCCTCGCCCTCCAGCTCAAGGTGGGACAAGTGCCCTAGAGTGCCCTGTGTCCAGGGACAGGCCC
CGCCTGGGTGCTGACATGCCCACCTCCATCTCTTCCCTCAGCACCTGAACCTCCTGGGGGGACCGTCA
GTCTTCCCTCTTCCCCCCTAAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAG
GTGCATCATGCCCAGACGAAGCCACGGGAGAGGCAGTTCAACAGCACGTACCGCGTGGTCAGCGTC
CTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGC
CTCCCGGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGTGGGACCCGCGGGGCCCGAGGGCCA
CGTGGACAGAGGCCGGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC
TACAGGGCAGCCCCGAGAGCCGCGAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAGAA
CCAGGTACAGCCTGACCTGCCTGGTTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAG
CAACGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGACGGCTCCTACTT
CCTCTACAGCAAGCTCATCGTGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGT
GATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA
(SEQ ID NO. 7)

cyno2-4cys amino acid sequence

ASTKGPSVFPLASCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTPPCPPCPAPELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWLNGKEYT
CKVSNKGLPAPIEKTISKAKGQPREPQVYILPPQEEELTKNQVSLTCLVTGFYPSDIAVEWESNGQ
PENTYKTTTPVLDSGYSFLYSLKLVDSRWQQGNTFSCSVMHLEALHNHYTQKSLSVSPGK
(SEQ ID NO. 8)

FIG. 4

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cynods1 genomic nucleotide sequence

GCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACAC
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTTCGTGGAACCTCAGGC
GCCCTGACCAGCGGCGTGACACCTTCCAGGCTGTCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACTCAGACCTACGTCTGCAACGTCGTTCATGAG
CCCAGCAACACCAAGGTCGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGAGGGGGAGTGTCTGCTG
GAAGCCATGCTCGGCCCTCCTGCCTGGACAAACCCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCGGTCTGTCTCCTCACCCAGAGGCCTCTGCCCCACCCCACTCATGCTCAGGGAGACAGTC
TTCTGGCTTTTTTCCACCAGACTCCGAGCAGGCACAGGCTGGATGCCCCCTACCCAGGCTCTGCACA
CATAGGGGCTGGTGTCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCCTGCTCCTGACCT
AAGCCCACCCCAAAGGCCAAACTCCACTCCCTCAGCTCGGAAACCTTCTCTCCTACCAGATCCCAG
TAACTCCCAATCTTCTCTCTGCAGAGTTTACACCCCCATGCCACCATGCCAGGTAAGCCAGCCC
AGGCCTCGCCCTCCAGCTCAAGGTGGGACAAGTGCCCTAGAGTGGCCTGTGTCCAGGGACAGGCCC
CGCCTGGGTGCTGACATGCCACCTCCATCTCTTCTCAGCACCTGAACTCCTGGGGGGACCGTCA
GTCTTCTCTTCCCCCCTAAACCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGC
GTGGTGGTGGACGTGAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAG
GTGCATCATGCCAGACGAAGCCACGGGAGAGGCAGTTCAACAGCACGTACCGCGTGGTCAGCGTC
CTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGGC
CTCCCGGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGTGGGACCCGCGGGGCCCCGAGGGCCA
CGTGGACAGAGGCCGGCTCAGCCCACCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCC
TACAGGGCAGCCCCGAGAGCCGAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAGAA
CCAGGTCAGCCTGACCTGCCTGGTCACAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAG
CAACGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGTGGACTCCGACGGCTCCTACTT
CCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGT
GATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAA
(SEQ ID NO. 9)

cynods1 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTPPCPPCPAPELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHHAQTKPRERQFNSTYRVVSVLTVTHQDWLNGKEYT
CKVSNKGLPAPIEKTISKAKGQPREPQVYILPPQEEELTKNQVSLTCLVTGFYPSDIAVEWESNGQ
PENTYKTTTPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK
(SEQ ID NO. 10)

FIG. 5

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cyno439 cDNA nucleotide sequence

CGTCTCTAGTGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGTGTCTGCTCCAGGAGCACCTC
CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCGTG
GAACTCAGGCGCCCTGACCAGCGGCGTGACACACCTTCCCGGCTGTCTTACAGTCCTCAGGGCTCTA
CTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGT
CGTTCATGAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTTCACACGCCCATGTGATGACAC
AACTCCCCCATGCCCACCGTGCCCGAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTTCGTCTTCCC
CCCAAACCCAAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGT
GAGCCAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAATGCCCA
GACGAAGCCGCGGGAGAGGCAGTTCAACAGCACATATCGTGTGGTTCAGCGTCTCACCCTCACGCA
CCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCAT
CCAGAAAACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTC
CCGGGAGGAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGA
CATCGTCTGTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACGCCGCCCGTGCT
GGACTCCGACGGCTCCTACTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG
GAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTC
CCTGTCTCCGGGTAAATGAGTCGACATGC (SEQ ID NO. 11)

cyno439 amino acid sequence

VSSASTKGPSVFPLVSCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY
SLSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTRPCDDTTPPCPPCPAPELLGGPSVVFVP
PKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAQTKPRERQFNSTYRVVSVLTVTH
QDWLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSD
IVVEWESSGQPENTYKTTTPVLDSDGSYFLYSKLTVDKSRWQQGNVFSQSVMHENHNHYTQKSLS
LSPGK (SEQ ID NO. 12)

FIG. 6

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cyno686 cDNA nucleotide sequence

CGTCTCTAGTCCACCAAGGGCCCATCGGTCTTCCCCCTGGTGTCTGCTCCAGGAGCACCTCCGAG
AGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCTGTGGAAC
TCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTTACAGTCCTCAGGGCTCTACTCC
CTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTT
CATGAGCCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTTTACACGCCCATGTGATGACACAAC
CCCCCATGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCGTCTTCCCCCA
AAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGC
CAGGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGCGCGGAGGTGCATCATGCCCAGACG
AAGCCACGGGAGACGCAGTACAACAGCACATATCGTGTGGTCAGCGTCCTCACCGTCACGCACCAG
GACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAG
AAAACCATCTCCAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGG
GAGGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCACGCGACATC
GTCGTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACGCCGCCCGTGTGGAC
TCCGACGGCTCCTACTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC
GTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTG
TCTCCGGGTAAATGAGTCGACATGC (SEQ ID NO. 13)

cyno686 amino acid sequence

RL*STKGPSVFPLVSCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS
LSSVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVEFTRPCDDTTPPCPPCPAPELLGGPSVVFVFP
KPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQ
DWLNGKEYTCKVSNKALPAPIQKTIISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDI
VVEWESSGQNPENTYKTPPVLDSDGSYFLYSLKLTVDKSRWQQGNVFSQSVMHREALHNHYTQKSLSL
SPGK (SEQ ID NO. 14)

FIG. 7

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cyno35 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTTCGTGGAACCTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCAGGCTGTCTTACAGTCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACTCAGACCTACGTCTGCAACGTTCGTTTCATGAG
CCCAGCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCGAGGGAAGGGGGGTGTCTGCTG
GAAGCCAGGCTCGGCCCTCCTGCCTGGACAACTCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCCGTCTGTCTTCTCACCCAGAGGCCTCTGCCCCACCCACTCATGCTCAGGGAGCCAGTC
TTCTGGCTTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCCTACCCAGGCCCTGCACA
CACAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA
AGCCACCCCAAAGGCCAACTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCCACATCCCAGT
AACTCCCAATCTTCTCTCTGTCAGGGCTCCCATGTTCGTTCCACGTGCCACCCGTGCCCAGGTAAGCC
AGCCAGGCCTCACCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA
GGCCCTGCCCGGGTGTGACACGTCCACCTCCATCTCTTCTCAGCTGAACCTGGGGGGACCGT
CAGTCTTCTCTTCCCCCCTAAACCCAAAGGACACCTCATGATTTCCCGGACCCCTGAGGTCACGT
GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCACAATGCCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG
TCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAG
CCCTCCCGGCCCAAAGCAGAAACTGTCTCCAAAACCAAAGGTGGGACCCGCGGGGCACGAGGGC
CACGTGGACAGAGGCCGGCTCAGCCACCCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC
CCTACAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAG
AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGTCGTGGAGTGGGAG
AGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCGCCCCGTGCTGGACTCCGACGGCTCCTAC
TTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA
(SEQ ID NO. 15)

cyno35 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKTVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVDVDSQEEPDKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY
TCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVVEWESSG
QPENTYKTTTPVLDSGYSFLYSLKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK*
(SEQ ID NO. 16)

FIG. 8

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cyno36 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTTCGTGGAACCTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCAGGCTGTCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCGTTTCATGAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGAAGGGGGGTGTCTGCTG
GAAGCCAGGCTCGGCCCTCCTGCCTGGACAACTCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCCGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC
TTCTGGCTTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCTACCCAGGCCCTGCACA
CACAGGGGCAGGTGCTGGGCTCAGACCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA
AGCCACCCCCAAAGGCCAACTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCACATCCCAGT
AACTCCCAATCTTCTCTCTGTCAGGGCTCCCATGTCTGTTCCACGTGCCACCGTGCCAGGTAAGCC
AGCCAGGCCTCACCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA
GGCCCTGCCCAGGTGCTGACACGTCCACCTCCATCTCTTCTCAGCTGAACTCCTGGGGGGACCGT
CAGTCTTCTCTTCCCCCAAAACCCAAGGACACCCTCATGATTTCCCGGACCCCTGAGGTCACGT
GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCACAATGCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG
TCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAG
CCCTCCCGGCCCAAGCAGAAAACCTGTCTCCAAAACCAAGGTGGGACCCGCGGGGCACGAGGGC
CACGTGGACAGAGGCCGCTCAGCCCACCCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC
CCTACAGGGCAGCCCCGAGAGCCACAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAG
AACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGTCGTGGAGTGGGCG
AGCAACGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGACGGCTCCTAC
TTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA
(SEQ ID NO. 17)

cyno36 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY
TCKVSNKALPAPKQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLVKGFYPSDIVEWASNG
QPENTYKTTTPVLDSDGSYFLYSKLTVDKSRWQQGNTFSCSVMHEALHNHYTQKSLSVSPGK*
(SEQ ID NO. 18)

FIG. 9

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cyno477 cDNA nucleotide sequence

TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACAGCG
GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCTGGAAGTCAAGGCGCC
CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTTACAGTCCTCAGGGCTCTACTCCCTCAGCAGC
GTGGTGACCGTGCCCTCCAGCAGCTTGGGACCCAGACCTACGTCTGCAACGTGTTTCATGAGCCC
AGCAACACCAAGGTGGACAAGACAGTTGGGCTCCCATGTCTGTTCCACGTGCCCACCGTGCCCAGCT
GAACTCCTGGGGGGACCGTCAGTCTTTCCTCTTCCCCCAAAACCCAAGGACACCTCATGATTTCC
CGGACCCCTGAGGTCACGTGCGTGGTGGTGGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAAC
TGGTACGTGGACGGCGTGGAGGTGCACAATGCCAGACAAAGCCGCGGGAGGAGCAGTTCAACAGC
ACGTATCGCGTGGTCAGCGTCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACG
TGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCAAGGCAGAAAACGTCTCCAAAACCAAGGGCAG
CCCCGAGAGCCGAGGTGTACACCCTGCCCCCGCCCCGGGAGGAGCTGACCAAGAACCAGGTCAGC
CTGACCTGCCTGATCAAAGGCTTCTACCCCAGCGACATCGTCGTGGAGTGGGCGAGCAACGGGCAG
CCGGAGAACACCTACAAGACCACGCCGCCCGTGCTGGACTCCGACGGCTCCTACTTCCTCTACAGC
AAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGTGATGCATGAG
GCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID
NO. 19).

cyno477 amino acid sequence

STKGPSVFPPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSS
VVTVPSSSLGTQTYVCNVVHEPSNTKVDKTVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMIS
RTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEYT
CKVSNKALPAPRQKTVSKTKGQPREPQVYTLPPPREELTKNQVSLTCLIKGFYPSDIVVEWASNGQ
PENTYKTTTPVLDSGYSFLYSLKLTVDKSRWQQGNTFSCSVMHREALHNHYTQKSLSLSPGK*
(SEQ ID NO. 20)

FIG. 10

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cyno32 genomic nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGTCCTGCTCCAGGAGCACCTCCCAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCCGTGACCGTGTCTGTGGAACCTCAGGC
GCCCTGACCAGCGCGTGCACACCTTCCAGGCTGTCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTCTGTCATGAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGGTGAGAGGCCAGCGAGGGGAGGGGGGTGTCTGCTG
GAAGCCAGGCTCGGCCCTCCTGCCTGGACAACTCTGGCTGTGCAGCCCCAGCCCAGGGCAGCAGG
GCAGGCCCCGTCTGTCTCCTCACCCAGAGGCCTCTGCCCACCCCACTCATGCTCAGGGAGCCAGTC
TTCTGGCTTTTTCCACCAGGCTCTGAGCAGGCACAGGCTGGATGCCCCTACCCCAGGCCCTGCACA
CACAGGGGCAGGTGCTGGGCTCAGGCCTGCCAAGAGCCATATCTGGGAGGACCCTGCCCTGACCTA
AGCCCACCCCAAAGGCCAACTCCACTCCCTCAGCTCAGACACCTTCTCTCCTCCACATCCCAGT
AACTCCCAATCTTCTCTCTGTCAGGGCTCCCATGTCTGTTCCACGTGCCACCGTGCCCAGGTAAGCC
AGCCCAGGCCTCACCTCCAGCTCAAGGTGGGACAAGCGCCCTAGAGTGGCCTGTGTCCAGGGACA
GGCCCTGCCCAGGTGCTGACACGTCCACCTCCATCTCTTCTCAGCTGAACTCCTGGGGGGACCGT
CAGTCTTCTCTTCCCCCCTCAAGGACACCTCATGATTTCCCGGACCCCTGAGGTCACGT
GCGTGGTGGTAGACGTGAGCCAGGAAGAACCCGATGTCAAGTTCAACTGGTACGTGGACGGCGTGG
AGGTGCACAATGCCAGACGAAGCCACGGGAGGAGCAGTTCAACAGCACGTACCGCGTGGTCAGCG
TCCTCACCGTCACACACCAGGACTGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAG
GCCTCCCGGCCCCCATCGAGAAAACCATCTCCAAGCCAAAGGTGGGACCCGCGGGGCCCCGAGGGC
CACGTGGACAGAGGCCGGCTCAGCCCACCTCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTC
CCTACAGGGCAGCCCCGAGAGCCGAGGTGTACATCCTGCCCCCGCCCCAGGAGGAGCTGACCAAG
AACCAGGTCAGCCTGACCTGCCTGGTCACAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAG
AGCAACGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGACGGCTCCTAC
TTCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGAACACCTTCTCATGCTCC
GTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCGTGTCTCCGGGTAAATGA
(SEQ ID NO. 21)

cyno32 amino acid sequence

ASTKGPSVFPLASCSRSTSQSTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFQAVLQSSGLYSLS
SVVTVPSSSLGTQTYVCNVVHEPSNTKVDKRVGLPCRSTCPPCPAELLGGPSVFLFPPKPKDTLMI
SRTPEVTCVVVDVSQEEPDVKFNWYVDGVEVHNAQTKPREEQFNSTYRVVSVLTVTHQDWLNGKEY
TCKVSNKGLPAPIEKTISKAKGQPREPQVYILPPQEEELTKNQVSLTCLVTGFYPSDIAVEWESNG
QPENTYKTTTPVLDSDGSYFLYSKLIVDKSRWQQGNTFSCSVMHLEAHNHYTQKSLSVSPGK*
(SEQ ID NO. 22)

FIG. 11

12/30

cyno3-18 cDNA nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCGTGGAACCTCAGGC
TCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAACATGTGGTGGTGGCAGCAAACCTCCCACG
TGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAACCC
AAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACGTGCGTGGTGGTAGACGTGAGCCAGGAA
GACCCCGATGTCAAGTTCAACTGGTACGTAAATGGCGCGGAGGTGCATCATGCCAGACGAAGCCA
CGGGAGACGCAGTACAACAGCACATATCGTGTGGTCAGCGTCTCACCGTCACGCACCAGGACTGG
CTGAACGGCAAGGAGTACAGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAAACC
ATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGGGAGGAG
CTGACCAAGAACCAGGTACGCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTCGTG
GAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGCTGGACTCCGAC
GGCTCCTACTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTC
TCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCTCCG
GGTAAA (SEQ ID NO. 23)

cyno3-18 amino acid sequence

ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGSLTSGVHTFPAVLQSSGLYSL
SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEITCGGSGSKPPTCPPCPAPELLGGPSVFLFPPKP
KDTLMISRTPEVTCVVVDVSQEDPDVKFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQDW
LNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIVV
EWESSGQPPENTYKTTTPVLDSDGSYFLYSLKLTVDKSRWQQGNVFSQSVMHENHNYTQKSLSLSP
GK (SEQ ID NO. 24)

FIG. 12

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cyno1-3 cDNA nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTCTGTGGAACCTCAGGC
GCCCTGACCAGCGGCGTGACACACCTTCCCGGCTGTCTTACAGTCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAAAAACATGTGGTGGTGGCAGCAAACCTCCC
ACGTGCCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCCAAAA
CCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAG
GAAGACCCCGAGGTCCAGTTCAACTGGTACGTAAACGGCGCGGAGGTGCATCATGCCCAGACGAAG
CCACGGGAGACGCAGTACAACAGCACGTACCGCGTGGTCAGCGTCCTCACCCTCACACACCAGGAC
TGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCCCATCCAGAAA
ACCATCTCCAAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGGGAG
GAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCCAGCGACATCGTC
GTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGTCTGGACTCC
GACGGCTCCTACTTCTCTACAGCAAGCTCACCCTGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCCAGAAGAGCCTCTCCCTGTCT
CCGGGTAAA (SEQ ID NO. 25)

cyno1-3 amino acid sequence

ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVEIKTCGGGSKPPTCPPCPAPELLGGPSVFLFPPK
PKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQD
WLNGKEYTCKVSNKALPAPIQKTISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIV
VEWESSGQPENTYKTTTPVLDSDGSYFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLS
PGK (SEQ ID NO. 26)

FIG. 13

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cyno1-4 cDNA nucleotide sequence

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTCCTCCAGGAGCACCTCCGAGAGCACA
GCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCTGAACCCGTGACCGTGTTCGTGGAACCTCAGGC
GCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCTTACAGTCCCTCAGGGCTCTACTCCCTCAGC
AGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACGTCTGCAACGTAAACCACAAG
CCCAGCAACACCAAGGTGGACAAGAGAGTTGAGATAAAAACATGTGGTGGTGGCAGCAAACCTCCC
ACGTGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCCTAAA
CCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCAG
GAAGACCCCGAGGTCCAGTTCAACTGGTACGTAAACGGCGCGGAGGTGCATCATGCCAGACGAAG
CCACGGGAGACGCAGTACAACAGCACGTACCGCGTGGTCAGCGTCCTCACCCTCACACACCAGGAC
TGGCTGAACGGCAAGGAGTACACGTGCAAGGTCTCCAACAAAGCCCTCCCGGCCCTCCATCCAGAAA
ACCATCTCCAAGACAAAGGGCAGCCCCGAGAGCCTCAGGTGTACACCCTGCCCCCGTCCCGGGAG
GAGCTGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGTC
GTGGAGTGGGAGAGCAGCGGGCAGCCGGAGAACACCTACAAGACCACCCCGCCCGTGTCTGGACTCC
GACGGCTCCTACTTCTCTACAGCAAGCTCACCCTGGGACAAGAGCAGGTGGCAGCAGGGGAACGTC
TTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACCAGAAGAGCCTCTCCCTGTCT
CCGGGTAAA (SEQ ID NO. 27)

cyno1-4 amino acid sequence

ASTKGPSVFPLAPSSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL
SVVTVPSSSLGTQTYVCNVNHKPSNTKVDKRVETKCGGSGKPPCTPPCPAPPELLGGPSVFLFPPK
PKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVNGAEVHHAQTKPRETQYNSTYRVVSVLTVTHQD
WLNKEYTCKVSNKALPAPIQKTIISKDKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIV
VEWESSGQPENTYKTTTPVLDSDGSYFLYSLKLTVDKSRWQQGNVFSQSVMHREALHNHYTQKLSLS
PGK (SEQ ID NO. 28)

FIG. 14

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cynoKappa cDNA nucleotide sequence

CGCGCTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGAGGATCAGGTGAAATCTGGA
ACTGTCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAGCGTAAAGTGGAAGGTGGAT
GGTGTCTCTCAAACGGGTAACTCCCAGGAGAGTGTTCACAGAGCAGGACAGCAAGGACAACACCTAC
AGCCTGAGCAGCACCCTGACGCTGAGCAGCACAGACTACCAGAGTCACAATGTCTATGCCTGCGAA
GTCACCCATCAGGGCCTGAGCTCGCCCGTCACCAAGAGCTTCAACAGAGGAGAGTGTTAGB
(SEQ ID NO. 29)

cynoKappa amino acid sequence

RAVAAPSVFIFPPSEDQVKSGTVSVVCLLNNFYPREASVKWKVDGVLKTGNSQESVTEQDSKDNTY
SLSSTLTLSSTDYQSHNVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO. 30)

FIG. 15

A. Nucleotide sequence alignments

16/30

_cyno33	GCCTCCACCAAGGGCCCATCGGTCTTCCCTCCGCGTCTGCTCCAGAGACCTCCCAAGACACAGGGGCCCTGGGCTGCCGTCAAGACTACTTCC	_cyno33
_cyno35	GCCTCCACCAAGGGCCCATCGGTCTTCCCTCCGCGTCTGCTCCAGAGACCTCCCAAGAGACAGGGGCCCTGGGCTGCCGTCAAGACTACTTCC	_cyno35
_cyno36	GCCTCCACCAAGGGCCCATCGGTCTTCCCTCCGCGTCTGCTCCAGAGACCTCCCAAGAGACAGGGGCCCTGGGCTGCCGTCAAGACTACTTCC	_cyno36
_cyno477	---TCCACCAAGGGCCCATCGGTCTTCCCTCCGCGTCTGCTCCAGAGACCTCCCAAGAGACAGGGGCCCTGGGCTGCCGTCAAGACTACTTCC	_cyno477
_cyno32	GCCTCCACCAAGGGCCCATCGGTCTTCCCTCCGCGTCTGCTCCAGAGACCTCCCAAGAGACAGGGGCCCTGGGCTGCCGTCAAGACTACTTCC	_cyno32

	110 120 130 140 150 160 170 180 190 200	
_cyno33	CCGAAACCGGTGACCGGTGTCGTGGAACCTCAGGCGCCCTGACAGGGCGGTGCAACACTTCAGGCTGTCTACAGTCTCAGGGCTCTACTCCCTCAGCAG	_cyno33
_cyno35	CCGAAACCGGTGACCGGTGTCGTGGAACCTCAGGCGCCCTGACAGGGCGGTGCAACACTTCAGGCTGTCTACAGTCTCAGGGCTCTACTCCCTCAGCAG	_cyno35
_cyno36	CCGAAACCGGTGACCGGTGTCGTGGAACCTCAGGCGCCCTGACAGGGCGGTGCAACACTTCAGGCTGTCTACAGTCTCAGGGCTCTACTCCCTCAGCAG	_cyno36
_cyno477	CCGAAACCGGTGACCGGTGTCGTGGAACCTCAGGCGCCCTGACAGGGCGGTGCAACACTTCGCGGTGTCTCAGTCTCAGGGCTCTACTCCCTCAGCAG	_cyno477
_cyno32	CCGAAACCGGTGACCGGTGTCGTGGAACCTCAGGCGCCCTGACAGGGCGGTGCAACACTTCAGGCTGTCTCAGTCTCAGGGCTCTACTCCCTCAGCAG	_cyno32

	210 220 230 240 250 260 270 280 290 300	
_cyno33	CGTGTGACCGGTGCCCTCCAGCAGGTGTGGGCACCTCAGACCTACGTCTGCAACGTCTCATGAGCCAGCAACACCAAGGTGGACACAGACAGTGGGCTC	_cyno33
_cyno35	CGTGTGACCGGTGCCCTCCAGCAGGTGTGGGCACCTCAGACCTACGTCTGCAACGTCTCATGAGCCAGCAACACCAAGGTGGACACAGACAGTGGGCTC	_cyno35
_cyno36	CGTGTGACCGGTGCCCTCCAGCAGGTGTGGGCACCTCAGACCTACGTCTGCAACGTCTCATGAGCCAGCAACACCAAGGTGGACACAGACAGTGGGCTC	_cyno36
_cyno477	CGTGTGACCGGTGCCCTCCAGCAGGTGTGGGCACCTCAGACCTACGTCTGCAACGTCTCATGAGCCAGCAACACCAAGGTGGACACAGACAGTGGGCTC	_cyno477
_cyno32	CGTGTGACCGGTGCCCTCCAGCAGGTGTGGGCACCTCAGACCTACGTCTGCAACGTCTCATGAGCCAGCAACACCAAGGTGGACACAGACAGTGGGCTC	_cyno32

	310 320 330 340 350 360 370 380 390 400	
_cyno33	CCATGTCGTTCCAGGTGCCACCGTGGCCAGCTGAACTCTCTGGGGGACCGTCAGTCTTCTCTTCCGCCCAAAACCAAGGACACCCCTCATGATTTCCC	_cyno33
_cyno35	CCATGTCGTTCCAGGTGCCACCGTGGCCAGCTGAACTCTCTGGGGGACCGTCAGTCTTCTCTTCCGCCCAAAACCAAGGACACCCCTCATGATTTCCC	_cyno35
_cyno36	CCATGTCGTTCCAGGTGCCACCGTGGCCAGCTGAACTCTCTGGGGGACCGTCAGTCTTCTCTTCCGCCCAAAACCAAGGACACCCCTCATGATTTCCC	_cyno36
_cyno477	CCATGTCGTTCCAGGTGCCACCGTGGCCAGCTGAACTCTCTGGGGGACCGTCAGTCTTCTCTTCCGCCCAAAACCAAGGACACCCCTCATGATTTCCC	_cyno477
_cyno32	CCATGTCGTTCCAGGTGCCACCGTGGCCAGCTGAACTCTCTGGGGGACCGTCAGTCTTCTCTTCCGCCCAAAACCAAGGACACCCCTCATGATTTCCC	_cyno32

FIG. 16A

17/30

	410	420	430	440	450	460	470	480	490	500	
_cyno33	GGACCCCTGAGGTCA	CGTGCCTGCTGTT	AGACGTGAGCC	AGGAGAA	ACCCGATGTC	CAAGTTCA	CGTGGAC	CGGCTGGAG	GTGCACA	ATGCCCA	_cyno33
_cyno35	GGACCCCTGAGGTCA	CGTGCCTGCTGTT	AGACGTGAGCC	AGGAGAA	ACCCGATGTC	CAAGTTCA	CGTGGAC	CGGCTGGAG	GTGCACA	ATGCCCA	_cyno35
_cyno36	GGACCCCTGAGGTCA	CGTGCCTGCTGTT	AGACGTGAGCC	AGGAGAA	ACCCGATGTC	CAAGTTCA	CGTGGAC	CGGCTGGAG	GTGCACA	ATGCCCA	_cyno36
_cyno477	GGACCCCTGAGGTCA	CGTGCCTGCTGTT	AGACGTGAGCC	AGGAGAA	ACCCGATGTC	CAAGTTCA	CGTGGAC	CGGCTGGAG	GTGCACA	ATGCCCA	_cyno477
_cyno32	GGACCCCTGAGGTCA	CGTGCCTGCTGTT	AGACGTGAGCC	AGGAGAA	ACCCGATGTC	CAAGTTCA	CGTGGAC	CGGCTGGAG	GTGCACA	ATGCCCA	_cyno32

	510	520	530	540	550	560	570	580	590	600	
_cyno33	GACGAAGCCACGG	AGGAGCAGTTTCA	ACAGCAGCTTAC	CGGCTGCTC	ACCGTCA	CACAC	CCAGGACT	TGGCTGA	ACCGCA	AGGAGTAC	CGTGC
_cyno35	GACGAAGCCACGG	AGGAGCAGTTTCA	ACAGCAGCTTAC	CGGCTGCTC	ACCGTCA	CACAC	CCAGGACT	TGGCTGA	ACCGCA	AGGAGTAC	CGTGC
_cyno36	GACGAAGCCACGG	AGGAGCAGTTTCA	ACAGCAGCTTAC	CGGCTGCTC	ACCGTCA	CACAC	CCAGGACT	TGGCTGA	ACCGCA	AGGAGTAC	CGTGC
_cyno477	GACGAAGCCACGG	AGGAGCAGTTTCA	ACAGCAGCTTAC	CGGCTGCTC	ACCGTCA	CACAC	CCAGGACT	TGGCTGA	ACCGCA	AGGAGTAC	CGTGC
_cyno32	GACGAAGCCACGG	AGGAGCAGTTTCA	ACAGCAGCTTAC	CGGCTGCTC	ACCGTCA	CACAC	CCAGGACT	TGGCTGA	ACCGCA	AGGAGTAC	CGTGC

*** *****

	610	620	630	640	650	660	670	680	690	700	
_cyno33	AAGTCTCCAAAG	CCCTCCCGCCCA	AAAGCAGAAA	ACTGTCT	CCAAA	ACCAAG	GGCAGCC	CCCGAGAG	CCACAG	GTGTAC	CCCTGCCCCCCCC
_cyno35	AAGTCTCCAAAG	CCCTCCCGCCCA	AAAGCAGAAA	ACTGTCT	CCAAA	ACCAAG	GGCAGCC	CCCGAGAG	CCACAG	GTGTAC	CCCTGCCCCCCCC
_cyno36	AAGTCTCCAAAG	CCCTCCCGCCCA	AAAGCAGAAA	ACTGTCT	CCAAA	ACCAAG	GGCAGCC	CCCGAGAG	CCACAG	GTGTAC	CCCTGCCCCCCCC
_cyno477	AAGTCTCCAAAG	CCCTCCCGCCCA	AAAGCAGAAA	ACTGTCT	CCAAA	ACCAAG	GGCAGCC	CCCGAGAG	CCACAG	GTGTAC	CCCTGCCCCCCCC
_cyno32	AAGTCTCCAAAG	CCCTCCCGCCCA	AAAGCAGAAA	ACTGTCT	CCAAA	ACCAAG	GGCAGCC	CCCGAGAG	CCACAG	GTGTAC	CCCTGCCCCCCCC

	710	720	730	740	750	760	770	780	790	800	
_cyno33	GGGAGGAGCTGAC	CAAGAAC	CAGGTGAG	CTGACCT	CGCTGCT	CAAGGCTT	CTACCC	ACGCA	ATCGT	CTGGAGT	GGCGAGCA
_cyno35	GGGAGGAGCTGAC	CAAGAAC	CAGGTGAG	CTGACCT	CGCTGCT	CAAGGCTT	CTACCC	ACGCA	ATCGT	CTGGAGT	GGCGAGCA
_cyno36	GGGAGGAGCTGAC	CAAGAAC	CAGGTGAG	CTGACCT	CGCTGCT	CAAGGCTT	CTACCC	ACGCA	ATCGT	CTGGAGT	GGCGAGCA
_cyno477	GGGAGGAGCTGAC	CAAGAAC	CAGGTGAG	CTGACCT	CGCTGCT	CAAGGCTT	CTACCC	ACGCA	ATCGT	CTGGAGT	GGCGAGCA
_cyno32	GGGAGGAGCTGAC	CAAGAAC	CAGGTGAG	CTGACCT	CGCTGCT	CAAGGCTT	CTACCC	ACGCA	ATCGT	CTGGAGT	GGCGAGCA

FIG. 16B

18/30

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      810      820      830      840      850      860      870      880      890      900
_cyno33  GAACACTACAAGACACCCCGCCCGTGTGGACTCCGACGGCTCCTACTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC _cyno33
_cyno35  GAACACTACAAGACACCCCGCCCGTGTGGACTCCGACGGCTCCTACTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC _cyno35
_cyno36  GAACACTACAAGACACCCCGCCCGTGTGGACTCCGACGGCTCCTACTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC _cyno36
_cyno477  GAACACTACAAGACACCCCGCCCGTGTGGACTCCGACGGCTCCTACTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC _cyno477
_cyno32  GAACACTACAAGACACCCCGCCCGTGTGGACTCCGACGGCTCCTACTTCTCTACAGCAAGCTCATCGTGGACAAGAGCAGGTGGCAGCAGGGGAAC _cyno32
*****
      910      920      930      940      950      960      970      980
_cyno33  ACCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACACCACTACACCCAGAGAGCCTCTCCGTGTCTCCGGGTAAA--- _cyno33
_cyno35  ACCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACACCACTACACCCAGAGAGCCTCTCCGTGTCTCCGGGTAAAATGA _cyno35
_cyno36  ACCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACACCACTACACCCAGAGAGCCTCTCCGTGTCTCCGGGTAAAATGA _cyno36
_cyno477  ACCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACACCACTACACCCAGAGAGCCTCTCCGTGTCTCCGGGTAAAATGA _cyno477
_cyno32  ACCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACACCACTACACCCAGAGAGCCTCTCCGTGTCTCCGGGTAAAATGA _cyno32
*****

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B. Nucleotide sequence alignments

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      cyno2-4  GCTAGCACCAGGGGCCATCGGTCTTCCCTGGCGTCTCTCCAGAGACACCTCCCGAGAGCAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCC _cyno4_2
      _cyno2-4cys  GCTAGCACCAGGGGCCATCGGTCTTCCCTGGCGTCTCTCCAGAGACACCTCCCGAGAGCAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCC _cyno4_2cys
      _cynods1  GCTAGCACCAGGGGCCATCGGTCTTCCCTGGCGTCTCTCCAGAGACACCTCCCGAGAGCAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCC _cyno2_4ds
      _cyno686  ---TCCAGCACCAGGGGCCATCGGTCTTCCCTGGCGTCTCTCCAGAGACACCTCCCGAGAGCAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCC _cyno686
      _cyno439  GCCTCCACCAGGGGCCATCGGTCTTCCCTGGCGTCTCTCCAGAGACACCTCCCGAGAGCAGCGGCCCTGGGCTGCTGGTCAAGGACTACTTCC _cyno439
      *****
      110      120      130      140      150      160      170      180      190      200
_cyno2-4  CCGAACCCGTGACTGTGTGTGGAACCTCAGGGCCCTGACAGGGCGTGCACACTTCCCGGTGTCTTACAGTCTCAGGGCTTACTCCCTCAGCAG _cyno4_2
      _cyno2-4cys  CCGAACCCGTGACTGTGTGTGGAACCTCAGGGCCCTGACAGGGCGTGCACACTTCCCGGTGTCTTACAGTCTCAGGGCTTACTCCCTCAGCAG _cyno4_2cys
      _cynods1  CCGAACCCGTGACTGTGTGTGGAACCTCAGGGCCCTGACAGGGCGTGCACACTTCCCGGTGTCTTACAGTCTCAGGGCTTACTCCCTCAGCAG _cyno2_4ds
      _cyno686  CCGAACCCGTGACTGTGTGTGGAACCTCAGGGCCCTGACAGGGCGTGCACACTTCCCGGTGTCTTACAGTCTCAGGGCTTACTCCCTCAGCAG _cyno686
      _cyno439  CCGAACCCGTGACTGTGTGTGGAACCTCAGGGCCCTGACAGGGCGTGCACACTTCCCGGTGTCTTACAGTCTCAGGGCTTACTCCCTCAGCAG _cyno439
      *****

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FIG. 16C

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cyno2-4      210      220      230      240      250      260      270      280      290      300      _cyno4_2
CGTGGTGACCGTGCCCTCCAGCAGCTTGGGGCACCAGACCTTACGCTCTGCAACGTCGTTTCATGAGCCAGCAACACCAGGTGGACAAGAGAGTTGAGTTTC
cyno2-4cys  CGTGGTGACCGTGCCCTCCAGCAGCTTGGGGCACCAGACCTTACGCTCTGCAACGTCGTTTCATGAGCCAGCAACACCAGGTGGACAAGAGAGTTGAGTTTC
cyno4_2cys  CGTGGTGACCGTGCCCTCCAGCAGCTTGGGGCACCAGACCTTACGCTCTGCAACGTCGTTTCATGAGCCAGCAACACCAGGTGGACAAGAGAGTTGAGTTTC
cyno2_4ds   CGTGGTGACCGTGCCCTCCAGCAGCTTGGGGCACCAGACCTTACGCTCTGCAACGTCGTTTCATGAGCCAGCAACACCAGGTGGACAAGAGAGTTGAGTTTC
cyno686     CGTGGTGACCGTGCCCTCCAGCAGCTTGGGGCACCAGACCTTACGCTCTGCAACGTCGTTTCATGAGCCAGCAACACCAGGTGGACAAGAGAGTTGAGTTTC
cyno439     CGTGGTGACCGTGCCCTCCAGCAGCTTGGGGCACCAGACCTTACGCTCTGCAACGTCGTTTCATGAGCCAGCAACACCAGGTGGACAAGAGAGTTGAGTTTC
*****
cyno2-4      310      320      330      340      350      360      370      380      390      400      _cyno4_2
ACAC-----CCCATGCCCCACCATGCCCCAGCACTTCTGCGGGGACCGCTCAGTCTTCTCTTCCCTCCCAAAACCCCAAGG
cyno2-4cys  ACAC-----CCCATGCCCCACCATGCCCCAGCACTTCTGCGGGGACCGCTCAGTCTTCTCTTCCCTCCCAAAACCCCAAGG
cynods1     ACAC-----CCCATGCCCCACCATGCCCCAGCACTTCTGCGGGGACCGCTCAGTCTTCTCTTCCCTCCCAAAACCCCAAGG
cyno686     ACACGCCCATGTGATGACACAACTCCCTCCCATGCCCCAGCGTGGCCAGCACTTGAACCTCTGCGGGGACCGCTCAGTCTTCTCTTCCCTCCCAAAACCCCAAGG
cyno439     ACACGCCCATGTGATGACACAACTCCCTCCCATGCCCCAGCGTGGCCAGCACTTGAACCTCTGCGGGGACCGCTCAGTCTTCTCTTCCCTCCCAAAACCCCAAGG
****
cyno2-4      410      420      430      440      450      460      470      480      490      500      _cyno4_2
ACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTCGAGCCAGGAAGACCCGAGAGTCCAGTTCAACTGGTTACGTGGACGGCGGT
cyno2-4cys  ACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTCGAGCCAGGAAGACCCGAGAGTCCAGTTCAACTGGTTACGTGGACGGCGGT
cynods1     ACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTCGAGCCAGGAAGACCCGAGAGTCCAGTTCAACTGGTTACGTGGACGGCGGT
cyno686     ACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTCGAGCCAGGAAGACCCGAGAGTCCAGTTCAACTGGTTACGTGGACGGCGGT
cyno439     ACACCCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTCGAGCCAGGAAGACCCGAGAGTCCAGTTCAACTGGTTACGTGGACGGCGGT
*****
cyno2-4      510      520      530      540      550      560      570      580      590      600      _cyno4_2
GGAGGTGCATCATGCCCCAGACGAAAGCCACGGGAGAGGCACTTCAACAGCACGTCACGCGTGGTTCAGCGCTCTTCCCTCACCCTCACACACCGAGACTGGGCTGAAC
cyno2-4cys  GGAGGTGCATCATGCCCCAGACGAAAGCCACGGGAGAGGCACTTCAACAGCACGTCACGCGTGGTTCAGCGCTCTTCCCTCACCCTCACACACCGAGACTGGGCTGAAC
cynods1     GGAGGTGCATCATGCCCCAGACGAAAGCCACGGGAGAGGCACTTCAACAGCACGTCACGCGTGGTTCAGCGCTCTTCCCTCACCCTCACACACCGAGACTGGGCTGAAC
cyno686     GGAGGTGCATCATGCCCCAGACGAAAGCCACGGGAGAGGCACTTCAACAGCACGTCACGCGTGGTTCAGCGCTCTTCCCTCACCCTCACACCGAGACTGGGCTGAAC
cyno439     GGAGGTGCATCATGCCCCAGACGAAAGCCACGGGAGAGGCACTTCAACAGCACGTCACGCGTGGTTCAGCGCTCTTCCCTCACCCTCACACCGAGACTGGGCTGAAC
*****

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FIG. 16D

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        610      620      630      640      650      660      670      680      690      700
GGCAAGGAGTACACGTGCAAGGTTCTCCAAACAAGGSCCTCCCGGCCCCCAATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAGCCGAGGTGT      _cyno4_2
GGCAAGGAGTACACGTGCAAGGTTCTCCAAACAAGGSCCTCCCGGCCCCCAATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAGCCGAGGTGT      _cyno4_2cys
GGCAAGGAGTACACGTGCAAGGTTCTCCAAACAAGGSCCTCCCGGCCCCCAATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAGCCGAGGTGT      _cyno2_4ds
GGCAAGGAGTACACGTGCAAGGTTCTCCAAACAAGGSCCTCCCGGCCCCCAATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAGCCGAGGTGT      _cyno686
GGCAAGGAGTACACGTGCAAGGTTCTCCAAACAAGGSCCTCCCGGCCCCCAATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAGCCGAGGTGT      _cyno439
*****
        710      720      730      740      750      760      770      780      790      800
ACATCTCTGCCCCCGCCAGGAGGAGTGTACCAAGAACCAGGTCAGCCTGACCTGCTGCTGCTCAAGGCTTCTACCCAGCGCATCGCCGTGGAGTGGGA      _cyno4_2
ACATCTCTGCCCCCGCCAGGAGGAGTGTACCAAGAACCAGGTCAGCCTGACCTGCTGCTGCTCAAGGCTTCTACCCAGCGCATCGCCGTGGAGTGGGA      _cyno4_2cys
ACATCTCTGCCCCCGCCAGGAGGAGTGTACCAAGAACCAGGTCAGCCTGACCTGCTGCTGCTCAAGGCTTCTACCCAGCGCATCGCCGTGGAGTGGGA      _cyno2_4ds
ACACCTCTGCCCCCGCTCCCGGGAGGAGTGTACCAAGAACCAGGTCAGCCTGACCTGCTGCTGCTCAAGGCTTCTACCCAGCGCATCGCTCTGCTGGAGTGGGA      _cyno686
ACACCTCTGCCCCCGCTCCCGGGAGGAGTGTACCAAGAACCAGGTCAGCCTGACCTGCTGCTGCTCAAGGCTTCTACCCAGCGCATCGCTCTGCTGGAGTGGGA      _cyno439
*** *****
        810      820      830      840      850      860      870      880      890      900
GAGCAACCGGGCAGCCGGGAGAACCTTACAGAACCAAGACCCCGCCGCTGCTGGACTCCGACGGCTCTACTTCTCTACAGCAAGCTCATCGTGGACAAGAGC      _cyno4_2
GAGCAACCGGGCAGCCGGGAGAACCTTACAGAACCAAGACCCCGCCGCTGCTGGACTCCGACGGCTCTACTTCTCTACAGCAAGCTCATCGTGGACAAGAGC      _cyno4_2cys
GAGCAACCGGGCAGCCGGGAGAACCTTACAGAACCAAGACCCCGCCGCTGCTGGACTCCGACGGCTCTACTTCTCTACAGCAAGCTCATCGTGGACAAGAGC      _cyno2_4ds
GAGCAGCGGGCAGCCGGGAGAACCTTACAGAACCAAGACCCCGCCGCTGCTGGACTCCGACGGCTCTACTTCTCTACAGCAAGCTCATCGTGGACAAGAGC      _cyno686
GAGCAGCGGGCAGCCGGGAGAACCTTACAGAACCAAGACCCCGCCGCTGCTGGACTCCGACGGCTCTACTTCTCTACAGCAAGCTCATCGTGGACAAGAGC      _cyno439
**** *****
        910      920      930      940      950      960      970      980      990
AGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACCTACACCCAGAGAGGCTCTCTCGTGTCTCCGGGTAAATGA      _cyno4_2
AGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACCTACACCCAGAGAGGCTCTCTCGTGTCTCCGGGTAAATGA      _cyno4_2cys
AGGTGGCAGCAGGGGAACACCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACCTACACCCAGAGAGGCTCTCTCGTGTCTCCGGGTAAATGA      _cyno2_4ds
AGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACCTACACCCAGAGAGGCTCTCTCGTGTCTCCGGGTAAATGA      _cyno686
AGGTGGCAGCAGGGGAACGCTTCTCATGCTCCGTGATGATGAGGCTCTGCACACCTACACCCAGAGAGGCTCTCTCGTGTCTCCGGGTAAATGA      _cyno439
*****

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FIG. 16E

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C. Nucleotide sequence alignments

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      10      20      30      40      50      60      70      80      90     100
_cyno3_18  GCCTCCACCAAGGGCCCATCGGTCTTCCCTTGGCGCCCTCTCCAGGAGCACCCTCGAGAGCACAGGGCCCTTGGGCTGCCCTGAGGACTACTTCC
_cyno3_16  GCCTCCACCAAGGGCCCATCGGTCTTCCCTTGGCGCCCTCTCCAGGAGCACCCTCGAGAGCACAGGGCCCTTGGGCTGCCCTGAGGACTACTTCC
_cyno1_3   GCCTCCACCAAGGGCCCATCGGTCTTCCCTTGGCGCCCTCTCCAGGAGCACCCTCGAGAGCACAGGGCCCTTGGGCTGCCCTGAGGACTACTTCC
_cyno1_4   GCCTCCACCAAGGGCCCATCGGTCTTCCCTTGGCGCCCTCTCCAGGAGCACCCTCGAGAGCACAGGGCCCTTGGGCTGCCCTGAGGACTACTTCC
*****

      110     120     130     140     150     160     170     180     190     200
_cyno3_18  CTGAACCCGTGACCGGTGTCGTGGAACTCAGGCTCCCTGACGAGGGCGTGCACACCTTCCCGGTGTCTTACAGTCTCTCAGGGCTCTTACTCCTCAGCAG
_cyno3_16  CTGAACCCGTGACCGGTGTCGTGGAACTCAGGCTCCCTGACGAGGGCGTGCACACCTTCCCGGTGTCTTACAGTCTCTCAGGGCTCTTACTCCTCAGCAG
_cyno1_3   CTGAACCCGTGACCGGTGTCGTGGAACTCAGGCGCCCTGACGAGGGCGTGCACACCTTCCCGGTGTCTTACAGTCTCTCAGGGCTCTTACTCCTCAGCAG
_cyno1_4   CTGAACCCGTGACCGGTGTCGTGGAACTCAGGCGCCCTGACGAGGGCGTGCACACCTTCCCGGTGTCTTACAGTCTCTCAGGGCTCTTACTCCTCAGCAG
*****

      210     220     230     240     250     260     270     280     290     300
_cyno3_18  CGTGGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGACCTTACGTCTGCAACGTAAACCAAGCCCAAGCAACCAAGGTGGACAAGAGAGTTGAGATA
_cyno3_16  CGTGGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGACCTTACGTCTGCAACGTAAACCAAGCCCAAGCAACCAAGGTGGACAAGAGAGTTGAGATA
_cyno1_3   CGTGGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGACCTTACGTCTGCAACGTAAACCAAGCCCAAGCAACCAAGGTGGACAAGAGAGTTGAGATA
_cyno1_4   CGTGGTGACCGTGCCTCCAGCAGCTTGGGCAACCCAGACCTTACGTCTGCAACGTAAACCAAGCCCAAGCAACCAAGGTGGACAAGAGAGTTGAGATA
*****

      310     320     330     340     350     360     370     380     390     400
_cyno3_18  ---ACATGTGGTGGCAGCAACCTCCACGTGCCACGTCGCCACGTCGCCAGCAGCCTGAACTCTCTGGGGGAGCCGTCAGTCTTCTTCCCTCCCAAAACCCCA
_cyno3_16  AAAACATGTGGTGGCAGCAACCTCCACGTGCCACGTCGCCACGTCGCCAGCAGCCTGAACTCTCTGGGGGAGCCGTCAGTCTTCTTCCCTCCCAAAACCCCA
_cyno1_3   AAAACATGTGGTGGCAGCAACCTCCACGTGCCACGTCGCCACGTCGCCAGCAGCCTGAACTCTCTGGGGGAGCCGTCAGTCTTCTTCCCTCCCAAAACCCCA
_cyno1_4   AAAACATGTGGTGGCAGCAACCTCCACGTGCCACGTCGCCACGTCGCCAGCAGCCTGAACTCTCTGGGGGAGCCGTCAGTCTTCTTCCCTCCCAAAACCCCA
*****

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FIG. 16F

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_cyno3_18      410      420      430      440      450      460      470      480      490      500
AGGACACCCCTCATGATCTCCCGGACCCCTGAGTCACTGCGTGTGGTAGACGTGAGCCAGGAGACCCCGATGTCAAGTTCACTGTACGTAATGG      _cyno3_18
AGGACACCCCTCATGATCTCCCGGACCCCTGAGTCACTGCGTGTGGTAGACGTGAGCCAGGAGACCCCGATGTCAAGTTCACTGTACGTAATGG      _cyno3_16
AGGACACCCCTCATGATCTCCCGGACCCCTGAGTCACTGCGTGTGGTAGACGTGAGCCAGGAGACCCCGATGTCAAGTTCACTGTACGTAATGG      _cyno1_3
AGGACACCCCTCATGATCTCCCGGACCCCTGAGTCACTGCGTGTGGTAGACGTGAGCCAGGAGACCCCGATGTCAAGTTCACTGTACGTAATGG      _cyno1_4
*****
_cyno3_18      510      520      530      540      550      560      570      580      590      600
CGCGAGGTGCATCATGCCCCAGACGAGCCACGCGGAGACGAGTACAACAGCACATATCGTGTGTGTCAGCGTCTCAACCGTCACGACCCAGGACTGGCTG      _cyno3_18
CGCGAGGTGCATCATGCCCCAGACGAGCCACGCGGAGACGAGTACAACAGCACATATCGTGTGTGTCAGCGTCTCAACCGTCACGACCCAGGACTGGCTG      _cyno3_16
CGCGAGGTGCATCATGCCCCAGACGAGCCACGCGGAGACGAGTACAACAGCACATATCGTGTGTGTCAGCGTCTCAACCGTCACGACCCAGGACTGGCTG      _cyno1_3
CGCGAGGTGCATCATGCCCCAGACGAGCCACGCGGAGACGAGTACAACAGCACATATCGTGTGTGTCAGCGTCTCAACCGTCACGACCCAGGACTGGCTG      _cyno1_4
*****
_cyno3_18      610      620      630      640      650      660      670      680      690      700
AACGCAAGGAGTACACGTGCAAGTCTTCCACAAAGCCCTCCCGCCCTCCATCCAGAAACCATCTCCAAAGACAAGGGCAGGCCCGAGAGCCTCAGG      _cyno3_18
AACGCAAGGAGTACACGTGCAAGTCTTCCACAAAGCCCTCCCGCCCTCCATCCAGAAACCATCTCCAAAGACAAGGGCAGGCCCGAGAGCCTCAGG      _cyno3_16
AACGCAAGGAGTACACGTGCAAGTCTTCCACAAAGCCCTCCCGCCCTCCATCCAGAAACCATCTCCAAAGACAAGGGCAGGCCCGAGAGCCTCAGG      _cyno1_3
AACGCAAGGAGTACACGTGCAAGTCTTCCACAAAGCCCTCCCGCCCTCCATCCAGAAACCATCTCCAAAGACAAGGGCAGGCCCGAGAGCCTCAGG      _cyno1_4
*****
_cyno3_18      710      720      730      740      750      760      770      780      790      800
TGTAACACCTGCCCCCGTCCCGGAGGAGTGAACCAAGACCCAGTCAAGCTGACCTGACCTGCTGCTCAAGGCTTCTACCCAGCGACATCGTCGTGGAGTG      _cyno3_18
TGTAACACCTGCCCCCGTCCCGGAGGAGTGAACCAAGACCCAGTCAAGCTGACCTGACCTGCTGCTCAAGGCTTCTACCCAGCGACATCGTCGTGGAGTG      _cyno3_16
TGTAACACCTGCCCCCGTCCCGGAGGAGTGAACCAAGACCCAGTCAAGCTGACCTGACCTGCTGCTCAAGGCTTCTACCCAGCGACATCGTCGTGGAGTG      _cyno1_3
TGTAACACCTGCCCCCGTCCCGGAGGAGTGAACCAAGACCCAGTCAAGCTGACCTGACCTGCTGCTCAAGGCTTCTACCCAGCGACATCGTCGTGGAGTG      _cyno1_4
*****

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FIG. 16G

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_cyno3_18      810      820      830      840      850      860      870      880      890      900
GGAGAGCAGCGGGGAGCCGGAGAACACCTTACAAGACCAACCCCGCCCGTGTGGACTCCGACGGCTCTTACTTCTCTTACAGCAAGCTCACCGTGGACAAG _cyno3_18
GGAGAGCAGCGGGGAGCCGGAGAACACCTTACAAGACCAACCCCGCCCGTGTGGACTCCGACGGCTCTTACTTCTCTTACAGCAAGCTCACCGTGGACAAG _cyno3_16
GGAGAGCAGCGGGGAGCCGGAGAACACCTTACAAGACCAACCCCGCCCGTGTGGACTCCGACGGCTCTTACTTCTCTTACAGCAAGCTCACCGTGGACAAG _cyno1_3
GGAGAGCAGCGGGGAGCCGGAGAACACCTTACAAGACCAACCCCGCCCGTGTGGACTCCGACGGCTCTTACTTCTCTTACAGCAAGCTCACCGTGGACAAG _cyno1_4
*****

_cyno3_18      910      920      930      940      950      960      970      980      990
AGCAGGTGGCAGCAGGGGGAACGTCCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACACCACTACACCCAGAGAGCCTCTCCCTCTCTCCGGGTAAA _cyno3_18
AGCAGGTGGCAGCAGGGGGAACGTCCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACACCACTACACCCAGAGAGCCTCTCCCTCTCTCCGGGTAAA _cyno3_16
AGCAGGTGGCAGCAGGGGGAACGTCCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACACCACTACACCCAGAGAGCCTCTCCCTCTCTCCGGGTAAA _cyno1_3
AGCAGGTGGCAGCAGGGGGAACGTCCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACACCACTACACCCAGAGAGCCTCTCCCTCTCTCCGGGTAAA _cyno1_4
*****
```

FIG. 16H

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AA sequence alignment

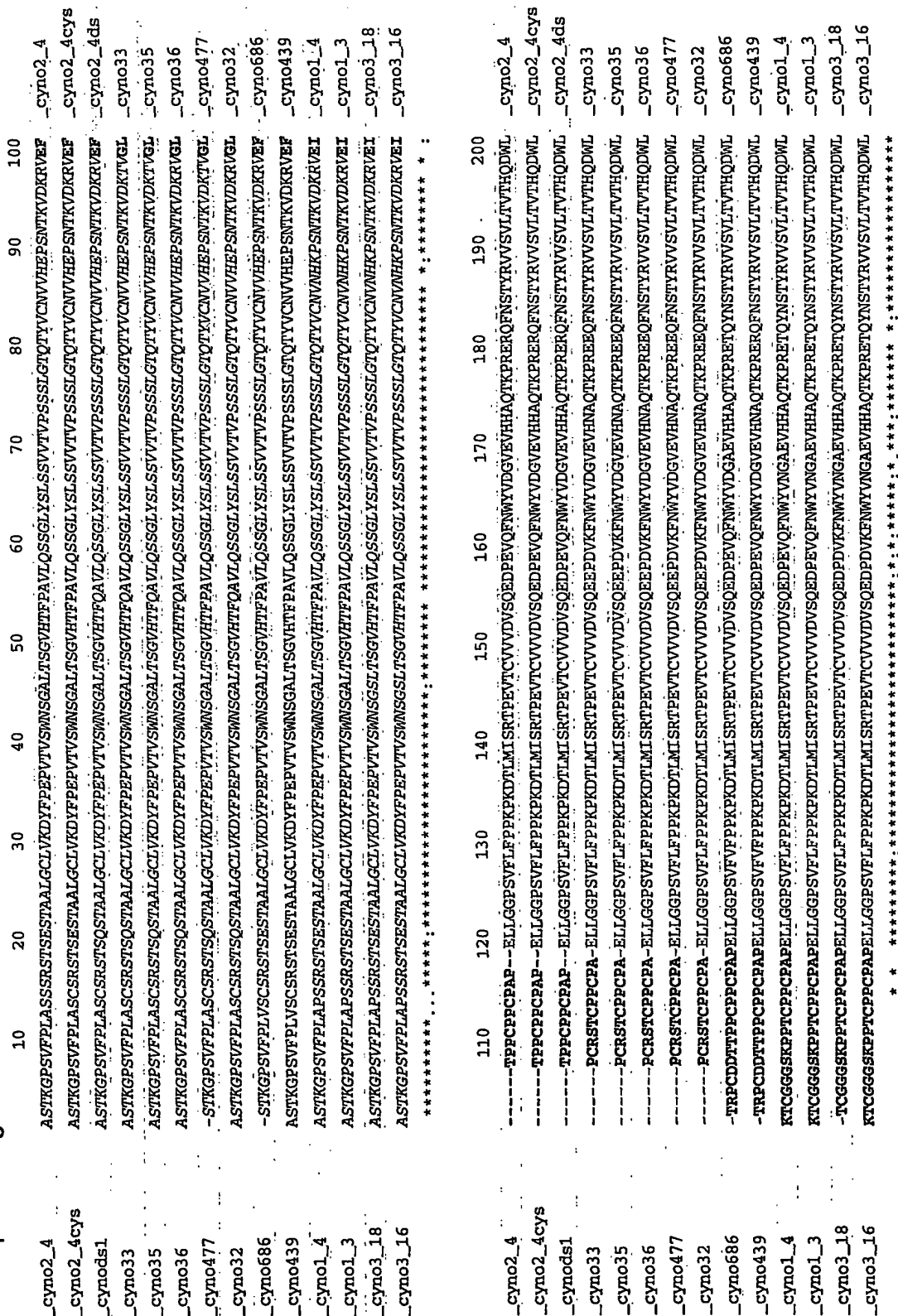


FIG. 17A

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A. Heavy Chain Variable Region Nucleotide Sequences

FR1									
H1	1	GAGGTTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H2	1	GAGGTTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H3	1	GAGGTTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H4	1	GAGGTTTCAGT	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H5	1	GAGGTTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H6	1	GAGGTTTCAGT	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H7	1	GAGGTTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H8	1	GAGGTTTCAGT	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H9	1	GAGGTTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H10	1	GAGGTTTCAGT	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H11	1	GAGGTTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H12	1	GAGGTTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H13	1	GAGGTTTCAGC	TGGTGCAGTC	TGGGGGAGGC	TTGGTACATC	CTGGGGGGGTC	CCTGAGACTC	60	
H14	1	GAGGTTTCAGT	TGGTGCAGTC	TGGGGGAGGC	TTGGTACAGC	CTGGGGGGGTC	CCTGAGACTC	60	
CDR1									
H1	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H2	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H3	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H4	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H5	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H6	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H7	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H8	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H9	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H10	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H11	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H12	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H13	61	TCCTGTGCAG	GCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
H14	61	TCCTGTGCAG	CCTCTGGATT	CACCTTCAGT	AGAAATGCTA	TGTTCTGGGT	TCGCCAGGCT	120	
FR2									
CDR2									
H1	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAACTATGCA	180	
H2	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180	
H3	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180	
H4	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAACTATGCA	180	
H5	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAACTATGCA	180	
H6	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAACTATGCA	180	
H7	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180	
H8	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAACTATGCA	180	
H9	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180	
H10	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAACTATGCA	180	
H11	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180	
H12	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180	
H13	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180	
H14	121	CCAGGAAAAG	GTCTGGAGTG	GGTATCAGGT	ATTGGTACTG	GTGGTGCCAC	AAGCTATGCA	180	

FIG. 18A

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										FR3	
H1	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H2	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H3	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H4	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H5	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H6	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H7	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H8	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H9	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H10	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H11	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H12	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H13	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H14	181	<u>GACTCCGTGA</u>	<u>AGGGCCGATT</u>	CACCATCTCC	AGAGACAATG	CCAAGAACTC	CTTGTATCTT	240			
H1	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H2	241	CAAATGAACA	GCCTGAGTGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H3	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H4	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H5	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H6	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H7	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H8	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H9	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H10	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H11	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H12	241	CAAATGAACA	GCCTGAGAGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H13	241	CAAATGAACA	GCCTGAGTGC	CGAGGACATG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
H14	241	CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCAAG	<u>AGGGAGGTAC</u>	300			
CDR3				FR4							
H1	301	<u>TACTTTGACT</u>	<u>ACTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:47)			
H2	301	<u>TACTTCACCC</u>	<u>ACTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:48)			
H3	301	<u>TGGTACAACA</u>	<u>ACTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:49)			
H4	301	<u>TACTTCCCGT</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:50)			
H5	301	<u>TACTTCACGA</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:51)			
H6	301	<u>TGGTACCCGT</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:52)			
H7	301	<u>TGGTACCCGT</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:53)			
H8	301	<u>TGGTTCCCGT</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:54)			
H9	301	<u>TGGTTCCCGT</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:55)			
H10	301	<u>TGGTACCCGT</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:56)			
H11	301	<u>TGGTACCCGT</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:57)			
H12	301	<u>TACTTCCCGT</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:58)			
H13	301	<u>TACTTCCCGT</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:59)			
H14	301	<u>TACTTCCCGT</u>	<u>GGTGGGGCCA</u>	GGGAACCCTG	GTCACCGTCT	CCTCA	345	(SEQ ID NO:60)			

FIG. 18B

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B. Heavy Chain Variable Region Amino Acid Sequences

	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4
H1	EVQLVQSGGGLVHPGSLRLSCAGSGFTFSRNAMFWVRQAPGKGLEWVSGIGTGGATNADSVKGRFTISRDNAKNSLYLQMNLSRAEDMAVYYCARGYYFDYWGQGLIVTVS						
H2	---	---	---	S---	S---	---	TH---
H3	---	---	---	S---	---	---	WYNN---
H4	---	---	---	---	---	---	PW---
H5	---	---	---	---	---	---	TR---
H6	---	---	---	---	---	---	YPW---
H7	---	---	---	S---	---	---	YPW---
H8	---	---	---	---	---	---	W-PW---
H9	---	---	---	S---	---	---	W-PW---
H10	---	---	---	---	---	---	WYFW---
H11	---	---	---	S---	---	---	WYFW---
H12	---	---	---	S---	---	---	PW---
H13	---	---	---	---	S---	---	PW---
H14	---	---	---	S---	---	---	T---

- H1 = (SEQ ID NO:61)
- H2 = (SEQ ID NO:62)
- H3 = (SEQ ID NO:63)
- H4 = (SEQ ID NO:64)
- H5 = (SEQ ID NO:65)
- H6 = (SEQ ID NO:66)
- H7 = (SEQ ID NO:67)
- H8 = (SEQ ID NO:68)
- H9 = (SEQ ID NO:69)
- H10 = (SEQ ID NO:70)
- H11 = (SEQ ID NO:71)
- H12 = (SEQ ID NO:72)
- H13 = (SEQ ID NO:73)
- H14 = (SEQ ID NO:74)

FIG. 18C

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A. Light Chain Variable Region Nucleotide Sequences

L1	1	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	AAGAGCCACC	60
L2	1	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	AAGAGCCACC	60
L3	1	GAAATTGTGT	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCGGGGGA	AAGAGCCACC	60
L4	1	GAAATTGTGA	TGACGCAGTC	TCCAGGCACC	CTGTCTTTGT	CTCCAGGGGA	AAGAGCCACC	60
L5	1	GATATTGTGC	TGACCCAGTC	TCCAGCCACC	CTGTCTTTGT	CTCCAGGGGA	AAGAGCCACC	60
L6	1	GATATTGTGC	TGACGCAGAC	TCCAGCCACC	CTGTCTTTGT	CTCCAGGGGA	AAGAGCCACC	60
CDR1								
L1	61	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTAGC	AGCAGCTACT	TAGCCTGGTA	CCAGCAGAAA	120
L2	61	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTAGC	AACAGCTACT	TAGCCTGGTA	CCAGCAGAAA	120
L3	61	CTCTCCTGCA	GGGCCAGTCA	GACTGTTAAC	AGCGACTACT	TAGCCTGGTA	CCAGCAGAAA	120
L4	61	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTAGC	AGCGACTACT	TAGCCTGGTA	CCAGCAGAAA	120
L5	61	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTAAC	AGCAACTACT	TAGCCTGGTA	CCAGCAGAAA	120
L6	61	CTCTCCTGCA	GGGCCAGTCA	GAGTGTTGGC	AGCAGCTACT	TAGCCTGGTA	CCAGCAGAGA	120
FR2								
CDR2								
L1	121	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTTT	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	180
L2	121	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	GGTGCATCCA	GCAGGGCCCC	TGGCATCCCA	180
L3	121	CCGGGCCAGG	CTCCCAGGCT	CCTCATCTAT	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCA	180
L4	121	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	GGTGCATCTA	GCAGGGCCTC	TGGCATCCCA	180
L5	121	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	GGTACATCCT	ACAGGGCCAC	TGGCATCCCA	180
L6	121	CCTGGCCAGG	CTCCCAGGCT	CCTCATCTAT	GGTGCATCCA	GCAGGGCCAC	TGGCATCCCG	180
FR3								
L1	181	GACAGGTTCA	GTGGCAGTGG	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	240
L2	181	GACAGGTTCA	GTGGCAGTGG	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	240
L3	181	GACAGGTTCA	GTGGCAGTGG	GTCTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	240
L4	181	GACAGGTTCA	GTGGCAGTGG	GTTTGGGACA	GACTTCACTC	TCACCATCAG	CAGACTGGAG	240
L5	181	GACAGGTTCA	GTGGCAGTGG	GTCTGGGACA	GACTTCACTC	TCACCATCAC	CAGACTGGAG	240
L6	181	GACAGGTTCA	GTGGCAGTGG	GTCTGGGACA	GACTTCACTC	TCACGATCAG	CAGACTGGAG	240
CDR3								
L1	241	CCTGAAGATT	TTGCAGTGTA	TTACTGTCAG	CAGTATGGTA	GCTCACCTCC	GTGGACGTTC	300
L2	241	CCTGAAGATT	TTGCAGTGTA	TTACTGTCAG	CAGTATGATC	ACTCAGCAGG	GTGGACGTTC	300
L3	241	CCTGAAGATT	TTGCAGTCTA	TTACTGTCAG	CAGTATGGTA	GGTCACCTCC	GTGGACGTTC	300
L4	241	CCTGAAGATT	TTGCAATATA	TTACTGTCAG	CAGTATGGTA	GCTCACCTCC	GTGGACGTTC	300
L5	241	CCTGAAGATT	TTGCAGTGTA	TTACTGTCAG	CAGTATGGTA	GCTCACCACT	GTGGACGTTC	300
L6	241	CCTGAAGATT	TTGCAGTGTA	TTATTGTCAG	CAGTATGGAA	GTTACACCTCC	GTGGATGTTC	300
FR4								
L1	301	GGCCAAGGGA	CCAAGGTGGA	AATCAAA	327 (SEQ ID NO:75)			
L2	301	GGCCAAGGGA	CCAAGGTGGA	GATCAAA	327 (SEQ ID NO:76)			
L3	301	GGCCAAGGGA	CCAAGGTGGA	TATCAAA	327 (SEQ ID NO:77)			
L4	301	GGCCAAGGGA	CCAAGGTGGA	AATCAAA	327 (SEQ ID NO:78)			
L5	301	GGCCAAGGGA	CACGACTGGA	GATTAAA	327 (SEQ ID NO:79)			
L6	301	GGCCAAGGGA	CCAAGGTGGA	GATCAAA	327 (SEQ ID NO:80)			

FIG. 19A

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B. Light Chain Variable Region Amino Acid Sequences

	FR1	CDR1	FR2	CDR2	FR3	CDR3	FR4	
L1	EIVLTQSPGTL	SLSPGERATL	SCRASQSVSSSYLA	WYQQKPGQAPRLLI	<u>FGASSRATGIP</u>	DRFSGSGSGTFTLTISRLEPEDFAVYYC	QQYGSPPWTFGQGT	KVEIK
L2	---	---	---	---	---	---	---	---
L3	---	---	---	---	---	---	---	---
L4	---	---	---	---	---	---	---	---
L5	D---	A---	N---	N---	---	---	---	---
L6	D---	T---	A---	G---	R---	---	---	---

- L1 = (SEQ ID NO:81)
- L2 = (SEQ ID NO:82)
- L3 = (SEQ ID NO:83)
- L4 = (SEQ ID NO:84)
- L5 = (SEQ ID NO:85)
- L6 = (SEQ ID NO:86)

FIG. 19B